

WEST Search History

DATE: Tuesday, February 08, 2005

Hide? Set Name Query**Hit Count***DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=AND*

<input type="checkbox"/>	L1	lee.in. or guerry.in. or burg.in.	259623
<input type="checkbox"/>	L2	L1 and (campylob\$ or campy\$)	89
<input type="checkbox"/>	L3	L2 and (plasmid or vector)	60
<input type="checkbox"/>	L4	L3 and (fla or fla-a or flaa or flagel\$ or SEQ or SEQ. or SEQ-ID).clm.	31
<input type="checkbox"/>	L5	L1 and (fla or fla-a or flaa or flagel\$ or SEQ or SEQ. or SEQ-ID).clm.	753
<input type="checkbox"/>	L6	L5 and (campyl\$ or campylobacter\$).clm.	1

END OF SEARCH HISTORY

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P27053

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[\[Entry info\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#)
[\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name **FLAA_CAMCO**
Primary accession number **P27053**
Secondary accession numbers None
Entered in Swiss-Prot in Release 23, August 1992
Sequence was last modified in Release 34, October 1996
Annotations were last modified in Release 44, July 2004

Name and origin of the protein

Protein name **Flagellin A**
Synonyms None
Gene name **Name: flaA**
From **Campylobacter coli [TaxID: 195]**
Taxonomy **Bacteria; Proteobacteria; Epsilonproteobacteria;
Campylobacterales; Campylobacteraceae; Campylobacter.**

References

[1] NUCLEOTIDE SEQUENCE.

STRAIN=VC167 T2;
MEDLINE=91310584;PubMed=1856171 [NCBI, ExPASy, EBI, Israel, Japan]
Guerry P., Alm R.A., Power M.E., Logan S.M., Trust T.J.;
"Role of two flagellin genes in Campylobacter motility.";
J. Bacteriol. 173:4757-4764(1991).

Comments

- **FUNCTION:** Flagellin is the subunit protein which polymerizes to form the filaments of bacterial flagella.
- **SUBUNIT:** Heteropolymer of flaA and flaB. A flagellar filament composed exclusively of flaA is indistinguishable in length from that of the wild type and shows a slight reduction in motility. The flagellar filament composed exclusively of the flaB is severely truncated in length and greatly reduced in motility. Thus, while both flagellins are not necessary for motility, both are required for a fully active flagellar filament.
- **SIMILARITY:** Belongs to the bacterial flagellin family.

Copyright

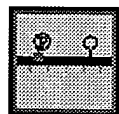
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Cross-references

EMBL M64670; AAA23022.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
 M64671; AAA23026.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
 PIR A42474; A42474.
 HSSP P06179; 1UCU. [HSSP ENTRY / PDB]
 IPR001029; Flagellin_C.
 InterPro IPR010810; Flagellin_IN.
 IPR001492; Flagellin_N.
 Graphical view of domain structure.
 Pfam PF00700; Flagellin_C; 1.
 PF07196; Flagellin_IN; 2.
 PF00669; Flagellin_N; 1.
 Pfam graphical view of domain structure.
 PRINTS PR00207; FLAGELLIN.
 ProDom PD000316; Flagellin_C; 1.
 [Domain structure / List of seq. sharing at least 1 domain]
 HOBACGEN [Family / Alignment / Tree]
 BLOCKS P27053.
 ProtoNet P27053.
 ProtoMap P27053.
 PRESAGE P27053.
 DIP P27053.
 ModBase P27053.
 SMR P27053; BD97DFF6CD099004.
 SWISS-2DPAGE Get region on 2D PAGE.
 UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

Flagellum.

Features

Feature table viewer

Key	From	To	Length	Description
INIT_MET	0	0		By similarity.
VARIANT	201	202	2	DS -> QN.

Sequence information

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 AA Da

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```

P27053 in FASTA
format

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BLAST

BLAST submission on
ExPASy/SIB
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)



ScanProsite, MotifScan



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Search for

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Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software.

In case of problems, please read the [online BLAST help](#).
If your question is not covered, please contact [<helpdesk@expasy.org>](mailto:helpdesk@expasy.org).

NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

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Query: 333 AA

Date run: 2005-02-08 16:27:35 UTC+0100 on elisio.isb-sib.ch

Program: NCBI BLASTP 2.2.6 [Apr-09-2003]

Database: /work/expasy/tmp/make_blast_fasta/UniProt

1,768,175 sequences; 565,733,592 total letters

UniProt Release 4.0 consists of: Swiss-Prot Release 46.0 of 01-Feb-2005: 168297 en
TrEMBL Release 29.0 of 01-Feb-2005: 1589670 entrie

Taxonomic view	NiceBlast view	Printable view
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List of potentially matching sequences

Send selected sequences to

☐ Include query sequence

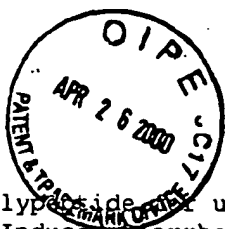
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SEQUENCE LISTING

<110> Guerry, Patricia
Trust, Trevor J
Burg, Edward
Lee, Lanfong



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Revised <141>

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O30688

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[\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name **O30688_CAMCO**
 Primary accession number **O30688**
 Secondary accession numbers None
 Entered in TrEMBL in Release 05, January 1998
 Sequence was last modified in Release 05, January 1998
 Annotations were last modified in Release 24, June 2003

Name and origin of the protein

Protein name **Flagellin A [Fragment]**
 Synonyms None
 Gene name **Name: flaA**
 From **Campylobacter coli [TaxID: 195]**
 Taxonomy **Bacteria; Proteobacteria; Epsilonproteobacteria;
 Campylobacterales; Campylobacteraceae; Campylobacter.**

References

- [1] NUCLEOTIDE SEQUENCE.
STRAIN=D1159;
 Meinersmann R.J., Helsel L.O., Fields P.I., Hiatt K.L.;
 "Discrimination of *Campylobacter jejuni* by fla gene sequencing."; *J. Clin. Microbiol.* 0:0-0(1997).

Comments

None

Cross-references

EMBL **AF015091; AAB69353.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]**
GO:0009420; Cellular component: flagellar filament (sensu Bacteria) (inferred from electronic annotation).
GO:0019861; Cellular component: flagellum (inferred from electronic annotation).
 GO **GO:0005198; Molecular function: structural molecule activity (inferred from electronic annotation).**
GO:0001539; Biological process: ciliary or flagellar motility (inferred from electronic annotation).

QuickGo
view.

InterPro IPR001492; Flagellin_N.
Graphical view of domain structure.

Pfam PF00669; Flagellin_N; 1.
Pfam graphical view of domain structure.

ProtoMap O30688.

PRESAGE O30688.

ModBase O30688.

SMR O30688; A1EBB1B61699B04D.

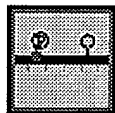
SWISS-2DPAGE Get region on 2D PAGE.

UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

Flagellum.

Features



Feature table viewer

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Sequence information

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O30688 in FASTA
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BLAST BLAST submission on
ExPASy/SIB
or at NCBI (USA)



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Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)



ScanProsite, MotifScan



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SV    M64670.1
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OC    Campylobacteraceae; Campylobacter.
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RX    PUBMED; 1856171.
RA    Guerry P., Alm R.A., Power M.E., Logan S.M., Trust T.J.;
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Entry information

Entry name **Q9WW79_CAMCO**
 Primary accession number **Q9WW79**
 Secondary accession numbers **None**
 Entered in TrEMBL in **Release 12, November 1999**
 Sequence was last modified in **Release 12, November 1999**
 Annotations were last modified in **Release 19, December 2001**

Name and origin of the protein

Protein name **Flagellin A [Fragment]**
 Synonyms **None**
 Gene name **Name: flaA**
 From **Campylobacter coli [TaxID: 195]**
 Taxonomy **Bacteria; Proteobacteria; Epsilonproteobacteria;
 Campylobacterales; Campylobacteraceae; Campylobacter.**

References

[1] NUCLEOTIDE SEQUENCE.

Studer E., Dohmke M., Wegmueller B., Luethy J., Schmid S., Candrian U.;
 "RFLP and sequence analysis of Campylobacter jejuni and Campylobacter coli PCR products
 amplified directly from environmental samples.";
 Food Sci. Technol. 31:337-345(1998).

[2] NUCLEOTIDE SEQUENCE.

Studer E.;
 Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

Comments

None

Cross-references

GO **GO:0019861; Cellular component: flagellum (inferred from electronic annotation).**
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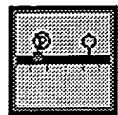
SWISS-2DPAGE Get region on 2D PAGE.

UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

Flagellum.

Features



Feature table viewer

Key	From	To	Length	Description
NON_TER	1	1		

Sequence information

Length: **14 AA** [This is the length of the partial sequence]

Molecular weight: **1611 Da** [This is the MW of the partial sequence]

CRC64: **C7C0EFB7A1739156** [This is a checksum on the sequence]

¹⁰
QANSVQQNVL RLLQ

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Dotlet (Java)



ScanProsite, MotifScan



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